```
<110> KAO CORPORATION
<120> Recombinant microorganisms
<130> KS0796
<150> JP 2003-379114
<151> 2003. 11. 7
<160> 22
<170> PatentIn Ver. 3.1
<210><211><211><211><212><213>
         1
3150
         DNA
         Bacillus sp. KSM-S237
         CDS
          (573).. (3044)
          sig_peptide
(573).. (659)
         mat_peptide (660)..()
<400> 1
gatttgccga tgcaacaggc ttatatttag aggaaatttc tttttaaatt gaatacggaa
                                                                                               60
taaaatcagg taaacaggtc cigattitat tittitgagt tittitagaga actgaagatt
                                                                                              120
gaaataaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac
                                                                                              180
                                                                                              240
gcctttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata
aaaccttata ttccggctct tttttaaaac agggggtaaa aattcactct agtattctaa
                                                                                              300
 tttcaacatg ctataataaa tttgtaagac gcaatatgca tctcttttt tacgatatat
                                                                                              360
gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta
                                                                                              420
gtaataatat agataactta taagtigitg agaagcagga gagcatcigg gitactcaca
                                                                                              480
agttttttta aaactttaac gaaagcactt teggtaatge ttatgaattt agetatttga
                                                                                              540
ttcaattact ttaaaaatat ttaggaggta at atg atg tta aga aag aaa aca
Met Met Leu Arg Lys Lys Thr
                                                                                              593
aag cag ttg att tct tcc att ctt att tta gtt tta ctt cta tct tta Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu -20
                                                                                              641
ttt ccg gca gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt
Phe Pro Ala Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe
-5 11
                                                                                              689
aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc
Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly
15 20 25
                                                                                              737
gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa
Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln
30 35
                                                                                              785
```

	V	VO 2	2005/	0450	45												P
cat His	gga Gly	gaa Glu 45	aaa Lys	att Ile	caa Gln	tta Leu	cgt Arg 50	gga Gly	atg Met	agt Ser	aca Thr	cac His 55	gga Gly	tta Leu	cag Gln	833	
tgg Trp	ttt Phe 60	cct Pro	gag Glu	atc Ile	ttg Leu	aat Asn 65	gat Asp	aac Asn	gca Ala	tac Tyr	aaa Lys 70	gct Ala	ctt Leu	tct Ser	aac Asn	881	
gat Asp 75	tgg Trp	gat Asp	tcc Ser	aat Asn	atg Met 80	att Ile	cgt Arg	ctt Leu	gct Ala	atg Met 85	tat Tyr	gta Val	ggt Gly	gaa Glu	aat Asn 90	929	
ggg Gly	tac Tyr	gct Ala	aca Thr	aac Asn 95	cct Pro	gag Glu	tta Leu	atc Ile	aaa Lys 100	caa Gln	aga Arg	gtg Val	att Ile	gat Asp 105	gga Gly	977	
att Ile	gag Glu	tta Leu	gcg Ala 110	att Ile	gaa Glu	aat Asn	gac Asp	atg Met 115	tat Tyr	gtt Val	att Ile	gtt Val	gac Asp 120	tgg Trp	cat His	1025	
gtt Val	cat His	gcg Ala 125	cca Pro	ggt Gly	gat Asp	cct Pro	aga Arg 130	gat Asp	cct Pro	gtt Val	tat Tyr	gca Ala 135	ggt Gly	gct Ala	aaa Lys	1073	ì
gat Asp	ttc Phe 140	ttt Phe	aga Arg	gaa Glu	att Ile	gca Ala 145	gct Ala	tta Leu	tac Tyr	cct Pro	aat Asn 150	aat Asn	cca Pro	cac His	att Ile	1121	
att Ile 155	tat Tyr	gag Glu	tta Leu	gcg Ala	aat Asn 160	gag Glu	ccg Pro	agt Ser	agt Ser	aat Asn 165	aat Asn	aat Asn	ggt Gly	gga Gly	gca Ala 170	1169	<del>)</del>
ggg Gly	att Ile	ccg Pro	aat Asn	aac Asn 175	Glu	gaa Glu	ggt Gly	tgg Trp	aaa Lys 180	gcg Ala	gta Val	aaa Lys	gaa Glu	tat Tyr 185	Ala	1217	7
gat Asp	cca Pro	att Ile	gta Val 190	Glu	atg Met	tta Leu	cgt Arg	aaa Lys 195	agc Ser	ggt Gly	aat Asn	gca Ala	gat Asp 200	Asp	aac Asn	1265	j
at t Ile	atc Ile	att Ile 205	Val	ggt Gly	agt Ser	cca Pro	aac Asn 210	Trp	agt Ser	cag Gln	cgt Arg	ccg Pro 215	Asp	tta Leu	gca Ala	1313	3
gc t Ala	gat Asp 220	Asn	cca Pro	att Ile	gat Asp	gat Asp 225	His	cat His	aca Thr	atg Met	tat Tyr 230	Thr	gtt Val	cac His	ttc Phe	136	1
tac Tyr 235	act Thr	gg t Gly	tca Ser	cat His	gct Ala 240	Ala	tca Ser	act Thr	gaa Glu	agc Ser 245	Tyr	ccg Pro	tct Ser	gaa Glu	act Thr 250	1409	9
cct Pro	aac Asn	tct Ser	gaa Glu	aga Arg 255	Gly	aac Asn	gta Val	atg Met	agt Ser 260	Asn	ac t Thi	cgt Arg	tat Tyr	gcg Ala 265	tta Leu	145	7
gaa Glu	aac Asn	gga Gly	gta Val 270	Ala	gta Val	ttt Phe	gca Ala	aca Thr 275	Glu	tgg Trp	gga	acg Thr	agt Ser 280	Gln	gct Ala	150	5
agt Sei	gga Gly	gac Asp 285	Gly	ggt Gly	cct Pro	tac Tyr	ttt Phe 290	Asp	gaa Glu	gca Ala	gat Asp	gta Val 295	Trp	att Ile	gaa Glu	155	3
tti Phe	tta Leu 300	Ast	gaa Glu	aac Asn	aac Asn	att Ile 305	Ser	tgg Trp	gct Ala	aac Asn	tgg Trr 310	) Ser	t t a	ace Thi	aat Asn	160	1
aaa Lys 315	s Asn	gaa Glu	gta Val	tct Ser	ggt Gly 320	' Ala	ttt Phe	aca Thr	cca Pro	tto Phe 325	: Glı	tta Leu	ggt	aag Lys	tct Ser 330	164	9

PCT/JP2004/016890

aac gc:WQ 20 Asn Ala Thr	Asn Leu Asp	cca ggt cca Pro Gly Pro	Asp His Val	tgg gca cca Trp Ala Pro		PCT/JP2004/016890
gaa tta agt	335 ctt tct gga Leu Ser Glv	gaa tat gta	cgt gct cgt	att aaa ggt Ile Lys Gly	gtg 1745	
	350	355		360		
aac tat gag Asn Tyr Glu 365	cca atc gac Pro Ile Asp	cgt aca aaa Arg Thr Lys 370	tac acg aaa Tyr Thr Lys	gta ctt tgg Val Leu Trp 375	gac 1793 Asp	
ttt aat gat Phe Asn Asp 380	gga acg aag Gly Thr Lys	caa gga ttt Gln Gly Phe 385	gga gtg aat Gly Val Asn 390	tcg gat tct Ser Asp Ser	cca 1841 Pro	
aat aaa gaa Asn Lys Glu 395	ctt att gca Leu Ile Ala 400	Val Asp Asn	gaa aac aac Glu Asn Asn 405	act ttg aaa Thr Leu Lys	gtt 1889 Val 410	
tcg gga tta Ser Gly Leu	gat gta agt Asp Val Ser 415	aac gat gtt Asn Asp Val	tca gat ggc Ser Asp Gly 420	aac ttc tgg Asn Phe Trp 425	gct 1937 Ala	·
Asn Ala Arg	ctt tct gcc Leu Ser Ala 430	aac ggt tgg Asn Gly Trp 435	gga aaa agt Gly Lys Ser	gtt gat att Val Asp Ile 440	tta 1985 Leu	
ggt gct gag Gly Ala Glu 445	aag ctt aca Lys Leu Thr	atg gat gtt Met Asp Val 450	att gtt gat Ile Val Asp	gaa cca acg Glu Pro Thr 455	acg 2033 Thr	1
gta gct att Val Ala Ile 460	gcg gcg att Ala Ala Ile	cca caa agt Pro Gln Ser 465	agt aaa agt Ser Lys Ser 470	gga tgg gca Gly Trp Ala	aat 2081 Asn	
cca gag cgt Pro Glu Arg 475	gct gtt cga Ala Val Arg 480	Val Asn Ala	gaa gat ttt Glu Asp Phe 485	gtc cag caa Val Gln Gln	acg 2129 Thr 490	
gac ggt aag Asp Gly Lys	tat aaa gct Tyr Lys Ala 495	gga tta aca Gly Leu Thr	att aca gga Ile Thr Gly 500	gaa gat gct Glu Asp Ala 505	cct 2177 Pro	,
Asn Leu Lys	aat atc gct Asn Ile Ala 510	ttt cat gaa Phe His Glu 515	gaa gat aac Glu Asp Asn	aat atg aac Asn Met Asn 520	aac 2225 Asn	i.
atc att ctg Ile Ile Leu 525	ttc gtg gga Phe Val Gly	act gat gca Thr Asp Ala 530	gct gac gtt Ala Asp Val	att tac tta Ile Tyr Leu 535	gat 2273 Asp	;
aac att aaa Asn Ile Lys 540	gta att gga Val Ile Gly	aca gaa gtt Thr Glu Val 545	gaa att cca Glu Ile Pro 550	gtt gtt cat Val Val His	gat 2321 Asp	
cca aaa gga Pro Lys Gly 555	gaa gct gtt Glu Ala Val 560	Leu Pro Ser	gtt ttt gaa Val Phe Glu 565	gac ggt aca Asp Gly Thr	cgt 2369 Arg 570	1
caa ggt tgg Gln Gly Trp	gac tgg gct Asp Trp Ala 575	gga gag tct Gly Glu Ser	ggt gtg aaa Gly Val Lys 580	aca gct tta Thr Ala Leu 585	aca 2417 Thr	,
lle Glu Glu	gca aac ggt Ala Asn Gly 590	tct aac gcg Ser Asn Ala 595	tta tca tgg Leu Ser Trp	gaa tit gga Glu Phe Gly 600	tat 2465 Tyr	i
cca gaa gta	aaa cct agt	gat aac tgg Asp Asn Trp 610	gca aca gct Ala Thr Ala	cca cgt tta Pro Arg Leu 615	gat 2513 Asp	3
	tct gac tig		gag aat gat	tat gta gct	ttt 2561	

Phe Trp Lys Sel Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe 620 625	PCT/JP2004/016890
gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile 635 640 650	2609
aat tta gta ttc cag cca cct act aac ggg tat tgg gta caa gca cca Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro 655 660 665	2657
aaa acg tat acg att aac ttt gat gaa tta gag gaa gcg aat caa gta Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val 670 675 680	2705
aat ggt tta tat cac tat gaa gtg aaa att aac gta aga gat att aca Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr 685 690 695	2753
aac att caa gat gac acg tta cta cgt aac atg atg atc att ttt gca Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala 700 705	2801
gat gta gaa agt gac ttt gca ggg aga gtc ttt gta gat aat gtt cgt Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg 715 720 730	2849
ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp 735 740 745	2897
cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu 750 760	2945
caa aaa gaa gca gag aaa gaa gag aaa gaa g	2993
aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys 780 785 790	3041
aaa taatctatta aactagttat agggttatct aaaggtctga tgtagatctt Lys 795	3094
ttagataacc tttttcttgc ataactggac acagagttgt tattaaagaa agtaag	3150
<pre>&lt;210&gt; 2 &lt;211&gt; 824 &lt;212&gt; PRT &lt;213&gt; Bacillus sp. KSM-S237</pre>	
<400> 2	
Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile Leu Ile -25 -20 -15	
Leu Val Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly -10 -1 1	
Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val	
Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly 20 35	

Gln Met WO 2005/045045 Sp Gln His Gly Glu Lys Ile Gln Leu Arg Gly 40 45 Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn 60 65 Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu 70 80 Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile 85 95 Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met 100 110 115 Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp 120 125 130 Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu 135 140 145 Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser 150 160 Ser Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp 165 170 Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys 180 185 190 195 Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His 225 Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr 230 240 Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met 245 255 Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr 260 275 Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp 285 290 Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp 295 300 305 Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr 310 320

Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro

Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val 340 355

Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys 360

Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe 375

Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn 390 400

Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val 415

Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp 420 435

Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val 440 450

Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser 455 460 465

Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala 470 480

Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr 485 490 495

Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu 510 515

Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala 520 525

Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val 535

Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser 550

Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser 575

Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala 580 595

Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp 600 605

Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly 625

Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala 630 640

Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn 645 655

Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu 660 675

Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys 680 685 690

Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg 695 700 705

Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg 710 720

Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
725 735

Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp 740 755

Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys 765 770

Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala 785

Val Lys Asn Glu Ala Lys Lys Lys 790 795

〈210〉 3 〈211〉 3332

<212≻ DNA <213≻ Bacillus sp. KSM-64

<220> <221> CDS <222> (610).. (3075)

<220> <221> sig\_peptide <222> (610)..(696)

<220> <221> mat\_peptide <222> (697)..() <223>

<400> 3
agtacttacc attttagagt caaaagatag aagccaagca ggatttgccg atgcaaccgg
cttatattta gagggaattt ctttttaaat tgaatacgga ataaaatcag gtaaacaggt
cctgatttta tttttttgaa tttttttgag aactaaagat tgaaatagaa gtagaagaca
180

acggacalaa 2005/045045 ttagttttaa ttatagaaaa cgcttttcta taattattta	240 PCT/JP2004/016890
tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc	300
ttttttaaa cagggggtga aaattcactc tagtattcta atttcaacat gctataataa	360
atttgtaaga cgcaatatac atctttttt tatgatattt gtaagcggtt aaccttgtgc	420
tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat	480
aagtigitga gaagcaggag agaatciggg tiacicacaa giitiitaaa acattaicga	540
aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta	600
ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile -25 -20	651
ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca Leu Ile Leu Val Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala -15 -10 -5 -1 1	699
gaa gga aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp 5 10 15	747
aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val 20 25 30	795
gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu 35 40 45	843
cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn 50 65	891
gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile 70 75 80	939
cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu 85 90 95	987
tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn 100 105	1035
gac atg tat gtc atc gtt gat tgg cat gta cat gca cct ggt gat cct Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro 115 120 125	1083
aga gat ccc gtt tac gct gga gca gaa gat ttc ttt aga gat att gca Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala 130 135 140 145	1131
gca tta tat cct aac aat cca cac att att tat gag tta gcg aat gag Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu 150 155 160	1179
cca agt agt aac aat aat ggt gga gct ggg att cca aat aat gaa gaa Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu 165 170 175	1227
ggt tgg aat gcg gta aaa gaa tac gct gat cca att gta gaa atg tta Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu 180 185 190	1275
cgt gat agc ggg aac gca gat gac aat att atc att gtg ggt agt cca Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro 195 200 205	1323

	V	VO 2	005/0	) <b>45</b> 04	15												PCT/JP2004/016890
aac Asn 210	Trp	agt Ser	cag Gln	cgt Arg	cct Pro 215	gac Asp	tta Leu	gca Ala	gct Ala	gat Asp 220	aat Asn	cca Pro	att Ile	gat Asp	gat Asp 225	1371	
cac His	cat His	aca Thr	atg Met	tat Tyr 230	ac t Thr	gtt Val	cac His	ttc Phe	tac Tyr 235	ac t Thr	ggt Gly	tca Ser	cat His	gct Ala 240	gct Ala	1419	
tca Ser	ac t Thr	gaa Glu	agc Ser 245	Tyr	ccg Pro	cct Pro	gaa Glu	ac t Thr 250	cct Pro	aac Asn	tct Ser	gaa Glu	aga Arg 255	gga Gly	aac Asn	1467	
gta Val	atg Met	agt Ser 260	Asn	ac t Thr	cgt Arg	tat Tyr	gcg Ala 265	tta Leu	gaa Glu	aac Asn	gga Gly	gta Val 270	gca Ala	gta Val	ttt Phe	1515	
gca Ala	aca Thr 275	gag Glu	tgg Trp	gga Gly	ac t Thr	agc Ser 280	caa Gln	gca Ala	aat Asn	gga Gly	gat Asp 285	ggt Gly	ggt Gly	cct Pro	tac Tyr	1563	
ttt Phe 290	Asp	gaa Glu	gca Ala	gat Asp	gta Val 295	tgg Trp	att Ile	gag Glu	ttt Phe	tta Leu 300	aat Asn	gaa Glu	aac Asn	aac Asn	att Ile 305	1611	
agc Ser	tgg Trp	gct Ala	aac Asn	tgg Trp 310	tct Ser	tta Leu	acg Thr	aat Asn	aaa Lys 315	aat Asn	gaa Glu	gta Val	tct Ser	ggt Gly 320	gca Ala	1659	
ttt Phe	aca Thr	cca Pro	ttc Phe 325	gag Glu	tta Leu	ggt Gly	aag Lys	tct Ser 330	aac Asn	gca Ala	aca Thr	agt Ser	ctt Leu 335	gac Asp	cca Pro	1707	
ggg Gly	cca Pro	gac Asp 340	caa Gln	gta Val	tgg Trp	gta Val	cca Pro 345	gaa Glu	gag Glu	tta Leu	agt Ser	ctt Leu 350	tct Ser	gga Gly	gaa Glu	1755	
tat Tyr	gta Val 355	cgt Arg	gct Ala	cgt Arg	att Ile	aaa Lys 360	ggt Gly	gtg Val	aac Asn	tat Tyr	gag Glu 365	cca Pro	atc Ile	gac Asp	cgt Arg	1803	
aca Thr 370	aaa Lys	tac Tyr	acg Thr	aaa Lys	gta Val 375	ctt Leu	tgg Trp	gac Asp	ttt Phe	aat Asn 380	gat Asp	gga Gly	acg Thr	aag Lys	caa Gln 385	1851	
gga Gly	ttt Phe	gga Gly	gtg Val	aat Asn 390	gga Gly	gat Asp	tct Ser	cca Pro	gtt Val 395	gaa Glu	gat Asp	gta Val	gtt Val	att Ile 400	gag Glu	1899	
aat Asn	gaa Glu	gcg Ala	ggc Gly 405	gct Ala	tta Leu	aaa Lys	ctt Leu	tca Ser 410	gga Gly	tta Leu	gat Asp	gca Ala	agt Ser 415	aat Asn	gat Asp	1947	
gtt Val	tct Ser	gaa Glu 420	ggt Gly	aat Asn	tac Tyr	tgg Trp	gct Ala 425	aat Asn	gct Ala	cgt Arg	ctt Leu	tct Ser 430	gcc Ala	gac Asp	ggt Gly	1995	
tgg Trp	gga Gly 435	aaa Lys	agt Ser	gtt Val	gat Asp	att Ile 440	tta Leu	ggt Gly	gct Ala	gaa Glu	aaa Lys 445	ctt Leu	ac t Thr	atg Met	gat Asp	2043	
gtg Val 450	att Ile	gtt Val	gat Asp	gag Glu	ccg Pro 455	acc Thr	acg Thr	gta Val	tca Ser	att Ile 460	gct Ala	gca Ala	att Ile	cca Pro	caa Gln 465	2091	
ggg Gly	cca Pro	tca Ser	gcc Ala	aat Asn 470	tgg Trp	gtt Val	aat Asn	Pro	aat Asn 475	cgt Arg	gca Ala	att Ile	Lys	gtt Val 480	gag Glu	2139	
cca Pro	act Thr	Asn	ttc Phe 485	gta Val	ccg Pro	tta Leu	Gly	gat Asp 490	aag Lys	ttt Phe	aaa Lys	Ala	gaa Glu 495	tta Leu	act Thr	2187	

ata act WQ 2005/045045ct cca tcg tta gaa gct att gcg atg cat gct Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala 500 505 510	2235 PCT/JP2004/016890
gaa aat aac aac atc aac atc att ctt ttt gta gga act gaa ggt Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly 515 520 525	2283
gct gat gtt atc tat tta gat aac att aaa gta att gga aca gaa gtt Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val 530 545	2331
gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt ctt cct tct Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser 550 555 560	2379
gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser 565 570 575	2427
ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala 580 585 590	2475
tta tca tgg gaa ttt gga tac cca gaa gta aaa cct agt gat aac tgg Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp 595 600 605	2523
gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly 610 615 620 625	2571
gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala 630 635 640	2619
aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn 645 650 655	2667
ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu 660 665 670	2715
tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys 675 680 685	2763
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg 690 700 705	2811
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg 710 715 720	2859
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro 725 730 735	2907
gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp 740 745 750	2955
gag aag gaa gcg aaa aaa gaa caa aaa gaa g	3003
gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala 770 775 780 785	3051
atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct	3105

## Ile LyWO 2005/045045 hr Lys Lys

aaaggtetga tgeagatett ttagataace tttttttgea taactggaca tagaatggtt 3165 attaaagaaa geaaggtgtt tataegatat taaaaaggta gegattttaa attgaaacet 3225 ttaataatgt ettgtgatag aatgatgaag taatttaaga gggggaaacg aagtgaaaac 3285 ggaaatttet agtagaagaa aaacagacea agaaatactg caagett 3332

- <210> 4
  <211> 822
- ⟨213⟩ Bacillus sp. KSM-64

<400> 4

Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile Leu Ile -25 -20 -15

Leu Val Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala Glu Gly
-10 -1 1

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly 20 35

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly 40 50

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu IIe Leu Asn Asp Asn 65

Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile Arg Leu 70 80

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu Leu Ile 85 95

Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn Asp Met 100 115

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp 120 125 130

Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp IIe Ala Ala Leu 135 145

Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser 150

Ser Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp 165

Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Asp 180 185 190 195 Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp 200 210

Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His 215 220

Thr Met Tyr Thr Val His Phe Tyr Thr Glv Ser His Ala Ala Ser Thr 230 240

Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met 245 255

Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr 260 265 270 275

Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr Phe Asp 280 285

Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp 295 300 305

Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr 310 320

Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro Gly Pro 325

Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val 340 355

Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys 360 370

Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe 375

Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu Asn Glu 390 400

Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp Val Ser 405

Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly Trp Gly 420 435

Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val Ile 440 450

Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln Gly Pro 455

Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu Pro Thr 470 475 480 Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr Ile Thr 485

Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala Glu Asn 500 505 510

Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly Ala Asp 520 530

Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile 545

Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe 550 560

Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val 565 575

Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser 580 595

Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr 600 605

Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn 615 625

Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu 630

Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr 645 655

Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu 660 675

Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn 680 690

Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met 695 705

Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe 710 720

Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu 725

Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys 740 750 755

Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala 765 770

Asn Glu Ala Thr Lys Lys 790

<210> 5 <211> 21 <212> DNA <213> Artificial Sequence

<400> 5

aaatgcgcaa aagatatgcg c 21

<210> 6 <211> 39 <212> DNA <213> Artificial Sequence

ctaatgggtg ctttagttgc tgataccgac gataatgcc 39

<210> 7
<211> 37
<212> DNA
<213> Artificial Sequence

ctgcccgtt agttgaagag actgccctcc ttttcgg 37

<210> 8 <211> 24 <212> DNA <213> Artificial Sequence

<400> 8

cgcaaactca taaaaatcat attt 24

<210> 9 <211> 26 <212> DNA <213> Artificial Sequence

caactaaagc acccattagt tcaaca 26

<210> 10 <211> 27 <212> DNA <213> Artificial Sequence

cttcaactaa cggggcaggt tagtgac 27

<210> 11 <211> 29 <212> DNA <213> Artificial Sequence

cagatgatat ggtgaaaaaa tcaaatccg 29

<210> 12 <211> 38

```
<212> LWO 2005/045045
<213> Artificial Sequence
<400> 12
gitatccgct cacaattccg agctgcatat cagatccc 38
<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence
<400> 13 cgtcgtgact gggaaaactg ttgattacaa agaggcag 38
<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence
<400> 14
ccatcggcca aatataagac acagccaacg c 31
<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence
<400> 15
gaattgtgag cggataac 18
<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence
<400> 16
gttttcccag tcacgacg 18
<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence
<400> 17
ataatgcccg cttcccaacc 20
<210> 18
<211> 38
<212> DNA
<213> Artificial Sequence
<400> 18
gttatccgct cacaattccg atcctcagct cctttgtc 38
<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence
<400> 19
cgtcgtgact gggaaaactc atctgatacc gattaacc 38
<210> 20
<211> 20
<212> DNA
```

## <213> AWO 2005/045045ence

<400> 20 caactgaatc cgaaggaatg 20

<210> <211> <212> <213>	21 2343 DNA Bacillus sp. pHSP-K38
<220><221><221><222><222><223>	CDS (580) (2067)
<220> <221> <222> <223>	sig_peptide (580) (627)
<220><221><222>	mat_peptide (628) ()

\2225 \223> <400> 21 agatctagca ggatttgccg atgcaaccgg cttatattta gagggaattt ctttttaaat 60 tgaatacgga ataaaatcag gtaaacaggt cctgatttta ttittttgaa tttttttgag 120 aactaaagat tgaaatagaa gtagaagaca acggacataa gaaaattgta ttagttttaa 180 ttatagaaaa cgcttttcta taattattta tacctagaac gaaaatactg tttcgaaagc 240 ggtttactat aaaaccttat attccggctc tttttttaaa cagggggtga aaattcactc 300 tagtatteta attteaacat getataataa atttgtaaga egeaatatae atetttttt 360 420 tatgatattt gtaageggtt aacettgtge tatatgeega ttlaggaagg gggtagattg agtcaagtag tcataattta gataacttat aagttgttga gaagcaggag agaatctggg 480 ttactcacaa gttttttaaa acattatcga aagcactttc ggttatgctt atgaatttag 540 ctatttgatt caattacttt aataatttta ggaggtaat atg atg tta aga aag Met Met Leu Arg Lys 594 aaa aca aag cag ttg ggt cga cca gca caa gcc gat gga ttg aac ggt Lys Thr Lys Gln Leu Gly Arg Pro Ala Gln Ala Asp Gly Leu Asn Gly -10 -5 1: 642 acg atg atg cag tat tat gag tgg cat ttg gaa aac gac ggg cag cat Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp Gly Gln His 10 20 690

tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat gct ggt att
Trp Asn Arg Leu His Asp Asp Ala Ala Leu Ser Asp Ala Gly Ile
25

aca gct att tgg att ccg cca gcc tac aaa ggt aat agt cag gcg gat
Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp
40

gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag ttc aat caa
Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln
55

aag ggt act gtt cga acg aaa tac gga act aag gca cag ctt gaa cga
Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg
70

882

gct Ala	ati <b>W</b> Ile	O 20 555 Gly	005/0 Ser	4504 Leu 90	āaa Lys	tct Ser	aat Asn	gat Asp	atc Ile 95	aat Asn	gta Val	tac Tyr	gga Gly	gat Asp 100	gtc Val	930 PCT/JP2004/0	16890
gtg Val	atg Met	aat Asn	cat His 105	aaa Lys	atg Met	gga Gly	gct Ala	gat Asp 110	ttt Phe	acg Thr	gag Glu	gca Ala	gtg Val 115	caa Gln	gct Ala	978	
gtt Val	caa Gln	gta Val 120	aat Asn	cca Pro	acg Thr	aat Asn	cgt Arg 125	tgg Trp	cag Gln	gat Asp	att Ile	tca Ser 130	ggt Gly	gcc Ala	tac Tyr	1026	
acg Thr	att Ile 135	gat Asp	gcg Ala	tgg Trp	acg Thr	ggt Gly 140	ttc Phe	gac Asp	ttt Phe	tca Ser	ggg Gly 145	cgt Arg	aac Asn	aac Asn	gcc Ala	1074	
tat Tyr 150	tca Ser	gat Asp	ttt Phe	aag Lys	tgg Trp 155	aga Arg	tgg Trp	ttc Phe	cat His	ttt Phe 160	aat Asn	ggt Gly	gtt Val	gac Asp	tgg Trp 165	1122	
gat Asp	cag Gln	cgc Arg	tat Tyr	caa Gln 170	gaa Glu	aat Asn	cat His	att Ile	ttc Phe 175	cgc Arg	ttt Phe	gca Ala	aat Asn	acg Thr 180	aac Asn	1170	
tgg Trp	aac Asn	tgg Trp	cga Arg 185	gtg Val	gat Asp	gaa Glu	gag Glu	aac Asn 190	ggt Gly	aat Asn	tat Tyr	gat Asp	tac Tyr 195	ctg Leu	tta Leu	1218	
gga Gly	tcg Ser	aat Asn 200	atc Ile	gac Asp	ttt Phe	agt Ser	cat His 205	cca Pro	gaa Glu	gta Val	caa Gln	gat Asp 210	gag Glu	ttg Leu	aag Lys	1266	
gat Asp	tgg Trp 215	ggt Gly	agc Ser	tgg Trp	ttt Phe	acc Thr 220	gat Asp	gag Glu	tta Leu	gat Asp	ttg Leu 225	gat Asp	ggt Gly	tat Tyr	cgt Arg	1314	
tta Leu 230	gat Asp	gct Ala	att Ile	aaa Lys	cat His 235	att Ile	cca Pro	ttc Phe	tgg Trp	tat Tyr 240	aca Thr	tct Ser	gat Asp	tgg Trp	gtt Val 245	1362	
cgg Arg	cat	cag Gln	cgc Arg	aac Asn 250	gaa Glu	gca Ala	gat Asp	caa Gln	gat Asp 255	Leu	ttt Phe	gtc Val	gta Val	ggg Gly 260	gaa Glu	1410	
tat Tyr	tgg Trp	aag Lys	gat Asp 265	gac Asp	gta Val	gg t Gly	gct Ala	ctc Leu 270	gaa Glu	ttt Phe	tat Tyr	tta Leu	gat Asp 275	gaa Glu	atg Met	1458	
aa t Asn	tgg Trp	gag Glu 280	Me t	tct Ser	cta Leu	t t c Phe	gat Asp 285	gtt Val	cca Pro	ctt Leu	aat Asn	tat Tyr 290	Asn	ttt Phe	tac Tyr	1506	
cgg Arg	gct Ala 295	tca Ser	caa Gln	caa Gln	ggt Gly	gga Gly 300	agc Ser	tat Tyr	gat Asp	atg Met	cgt Arg 305	Asn	att Ile	tta Leu	cga Arg	1554	
gga Gly 310	tct Ser	t t a Leu	gta Val	gaa Glu	gcg Ala 315	cat His	ccg Pro	atg Met	cat His	gca Ala 320	Val	acg Thr	ttt Phe	gtt Val	gat Asp 325	1602	
aa t Asn	cat His	gat Asp	ac t Thr	cag Gln 330	Pro	ggg Gly	gag Glu	tca Ser	tta Leu 335	Glu	tca Ser	tgg Trp	gtt Val	gct Ala 340	Asp	1650	
tgg Trp	ttt Phe	aag Lys	cca Pro 345	Leu	gct Ala	tat Tyr	gcg Ala	aca Thr 350	Ile	ttg Leu	acg Thr	cgt Arg	gaa Glu 355	Gly	ggt Gly	1698	
tat Tyr	cca Pro	aat Asn 360	Val	ttt Phe	tac Tyr	gg t Gly	gat Asp 365	Tyr	tat Tyr	ggg Gly	att	cct Pro 370	Asn	gat Asp	aac Asn	1746	
att	tca	gct	aaa	aaa	gat	atg	att	gat	gag	ctg	ctt	gat	gca	cgt	caa	1794	

Ile Se <b>WO 2005/045045</b> sp Met Ile Asp Glu Leu Leu Asp Ala Arg Gln 375 380 385	PCT/JP2004/016890
aat tac gca tat ggc acg cag cat gac tat ttt gat cat tgg gat gtt Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His Trp Asp Val 390 400 405	1842
gta gga tgg act agg gaa gga tct tcc tcc aga cct aat tca ggc ctt Val Gly Trp Thr Arg Glu Gly Ser Ser Arg Pro Asn Ser Gly Leu 410 415 420	1890
gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg atg tat gta Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp Met Tyr Val 425 430 435	1938
gga cgt cag aat gca gga caa aca tgg aca gat tta act ggt aat aac Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn 440 445 450	1986 .
gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa ttc ttt acg Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr 455 460 465	2034
aat gga gga tot gta too gtg tao gtg aac caa taacaaaaag cottgagaag Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln 470 475 480	2087
ggattcctcc ctaactcaag gctttcttta tgtcgcttag ctttacgctt ctacgacttt	2147
gaagettggg gateegtega gacaaggtaa aggataaaac agcacaatte caagaaaaac	2207
acgatttaga acctaaaaag aacgaatttg aactaactca taaccgagag gtaaaaaaaag	2267
aacgaagtcg agatcaggga atgagtttat aaaataaaaa aagcacctga aaaggtgtct	2327
ttttttgatg tctaga	2343
<210> 22 <211> 496 <212> PRT <213> Bacillus sp. pHSP-K38	
<400> 22 Met Met Leu Arg Lys Lys Thr Lys Gln Leu Gly Arg Pro Ala Gln Ala	
-15 -10 -5 -1	
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu 1 10 15	
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu 20 25 30	
Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly 35 40	
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 60	
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 75 80	
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn 85 90 95	

Val Ty. WO 2005/045045 al Met Asn His Lys Met Gly Ala Asp Phe Thr 100 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp 115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser 130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe 145 150 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg 165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn 180 185

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp 210 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr 225 230 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu 245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe 260 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu 275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met 290 295

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala 305 310 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu 325

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu 340 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly 355

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu 370

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe

385

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Arg 415

Pro Asn Ser Gly Leu Ala Thr IIe Met Ser Asn Gly Pro Gly Gly Ser 420

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp 435

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp 450